```
                      GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:         June 12, 2006, 20:28:58 ; Search time 184 Seconds
                                           (without alignments)
                                          271.887 Million cell updates/sec

Title:          US-10-680-800A-2
Perfect score:  599
Sequence:       1 MRSLCCAPLLLLLLLPPLLL..........LPGLACLRTSFNRFICLAQK 108

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:      2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :       Published_Applications_AA_Main:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
                %
Result          Query
  No.   Score   Match Length DB  ID                          Description
 ---------------------------------------------------------------------------
     1    599   100.0    108  4  US-10-016-481-5              Sequence 5, Appli
     2    599   100.0    108  4  US-10-231-411-4              Sequence 4, Appli
     3    599   100.0    108  4  US-10-212-355-2              Sequence 2, Appli
     4    599   100.0    108  4  US-10-323-157-5              Sequence 5, Appli
     5    599   100.0    108  4  US-10-212-201-2              Sequence 2, Appli
     6    599   100.0    108  4  US-10-467-019-17             Sequence 17, Appl
     7    599   100.0    108  4  US-10-680-755A-2             Sequence 2, Appli
     8    599   100.0    108  4  US-10-680-800A-2             Sequence 2, Appli
     9    599   100.0    108  5  US-10-713-567-5              Sequence 5, Appli
    10    599   100.0    108  5  US-10-811-328-5              Sequence 5, Appli
    11    599   100.0    108  5  US-10-912-907-5              Sequence 5, Appli
  12     599  100.0     108  5  US-10-415-724-5             Sequence 5, Appli
  13     599  100.0     108  5  US-10-990-246-2             Sequence 2, Appli
  14     599  100.0     108  5  US-10-503-554A-17           Sequence 17, Appl
  15     599  100.0     108  5  US-10-982-168-2             Sequence 2, Appli
  16     599  100.0     108  5  US-10-504-588-6             Sequence 6, Appli
  17     599  100.0     116  4  US-10-680-755A-26           Sequence 26, Appl
  18     599  100.0     116  4  US-10-680-800A-26           Sequence 26, Appl
  19     584   97.5     108  5  US-10-713-567-34            Sequence 34, Appl
  20     584   97.5     108  5  US-10-977-113-6             Sequence 6, Appli
  21     584   97.5     108  6  US-11-073-420-6             Sequence 6, Appli
  22   578.5   96.6     129  4  US-10-132-812-14            Sequence 14, Appl
  23   578.5   96.6     129  4  US-10-231-411-2             Sequence 2, Appli
  24   578.5   96.6     129  4  US-10-680-755A-29           Sequence 29, Appl
  25   578.5   96.6     129  4  US-10-680-800A-29           Sequence 29, Appl
  26   536.5   89.6     100  3  US-09-886-242A-4            Sequence 4, Appli
  27   536.5   89.6     100  4  US-10-027-603-4             Sequence 4, Appli
  28   536.5   89.6     100  5  US-10-692-299-4             Sequence 4, Appli
  29   531.5   88.7     107  4  US-10-467-019-37            Sequence 37, Appl
  30   531.5   88.7     107  4  US-10-362-504-69            Sequence 69, Appl
  31   531.5   88.7     107  5  US-10-503-554A-37           Sequence 37, Appl
  32   527.5   88.1     107  4  US-10-132-812-10            Sequence 10, Appl
  33   527.5   88.1     107  4  US-10-231-411-6             Sequence 6, Appli
  34   527.5   88.1     107  4  US-10-467-019-55            Sequence 55, Appl
  35   527.5   88.1     107  5  US-10-503-554A-55           Sequence 55, Appl
  36     461   77.0      81  4  US-10-016-481-6             Sequence 6, Appli
  37     461   77.0      81  4  US-10-323-157-6             Sequence 6, Appli
  38     461   77.0      81  4  US-10-417-426-5             Sequence 5, Appli
  39     461   77.0      81  4  US-10-467-019-19            Sequence 19, Appl
  40     461   77.0      81  5  US-10-680-554-7             Sequence 7, Appli
  41     461   77.0      81  5  US-10-713-567-6             Sequence 6, Appli
  42     461   77.0      81  5  US-10-811-328-6             Sequence 6, Appli
  43     461   77.0      81  5  US-10-912-907-6             Sequence 6, Appli
  44     461   77.0      81  5  US-10-415-724-6             Sequence 6, Appli
  45     461   77.0      81  5  US-10-977-113-9             Sequence 9, Appli
  46     461   77.0      81  5  US-10-871-152-18            Sequence 18, Appl
  47     461   77.0      81  5  US-10-503-554A-19           Sequence 19, Appl
  48     461   77.0      81  6  US-11-073-420-9             Sequence 9, Appli
  49     456   76.1      80  4  US-10-467-019-22            Sequence 22, Appl
  50     456   76.1      80  5  US-10-503-554A-22           Sequence 22, Appl
  51   454.5   75.9     118  4  US-10-132-812-8             Sequence 8, Appli
  52     450   75.1      81  6  US-11-073-420-37            Sequence 37, Appl
  53     445   74.3      81  4  US-10-417-426-7             Sequence 7, Appli
  54     445   74.3      81  4  US-10-467-019-39            Sequence 39, Appl
  55     445   74.3      81  4  US-10-362-504-71            Sequence 71, Appl
  56     445   74.3      81  5  US-10-680-554-9             Sequence 9, Appli
  57     445   74.3      81  5  US-10-680-554-11            Sequence 11, Appl
  58     445   74.3      81  5  US-10-713-567-29            Sequence 29, Appl
  59     445   74.3      81  5  US-10-713-567-31            Sequence 31, Appl
  60     445   74.3      81  5  US-10-811-328-29            Sequence 29, Appl


                              ALIGNMENTS


RESULT 1
US-10-016-481-5
; Sequence 5, Application US/10016481
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OM protein - protein search, using sw model

Run on:         June 12, 2006, 20:08:07 ; Search time 202 Seconds
                                           (without alignments)
                                          244.452 Million cell updates/sec

Title:          US-10-680-800A-2
Perfect score:  599
Sequence:       1 MRSLCCAPLLLLLLLPPLLL..........LPGLACLRTSFNRFICLAQK 108

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :       A_Geneseq_8:*
                1:  geneseqp1980s:*
                2:  geneseqp1990s:*
                3:  geneseqp2000s:*
                4:  geneseqp2001s:*
                5:  geneseqp2002s:*
                6:  geneseqp2003as:*
                7:  geneseqp2003bs:*
                8:  geneseqp2004s:*
                9:  geneseqp2005s:*
                10:  geneseqp2006s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                 %
Result           Query
   No.   Score   Match Length DB  ID                          Description
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     1     599   100.0    108  4  AAB68426                    Aab68426 Amino aci
     2     599   100.0    108  5  ABG94397                    Abg94397 Human GPC
     3     599   100.0    108  5  AAO15531                    Aao15531 Human phy
     4     599   100.0    108  5  AAE24384                    Aae24384 Human pro
     5     599   100.0    108  6  ABU07602                    Abu07602 Human ZVE
     6     599   100.0    108  6  AAE36789                    Aae36789 Human Bv8
     7     599   100.0    108  7  ADD69039                    Add69039 Human Bv8
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  8     599  100.0     108  7  ADF28067                   Adf28067 Human Zve
  9     599  100.0     108  7  ABG75087                   Abg75087 Human pro
 10     599  100.0     108  7  ADJ71811                   Adj71811 Human pro
 11     599  100.0     108  8  ADN41839                   Adn41839 Amino aci
 12     599  100.0     108  8  ADO24421                   Ado24421 Human PRO
 13     599  100.0     108  8  ADS86957                   Ads86957 Human Zve
 14     599  100.0     108  8  ADS00460                   Ads00460 Human Bv8
 15     599  100.0     108  8  ADS86495                   Ads86495 Human BV8
 16     599  100.0     108  8  ADS75496                   Ads75496 Human pro
 17     599  100.0     108  9  AEA23706                   Aea23706 Human PRO
 18     599  100.0     108  9  AEB45585                   Aeb45585 Human Zve
 19     599  100.0     108  9  AED08085                   Aed08085 Human Zve
 20     599  100.0     116  8  ADN41861                   Adn41861 Amino aci
 21     599  100.0     116  8  ADS86981                   Ads86981 Human Zve
 22     584   97.5     108  9  ADZ88897                   Adz88897 Rhesus mo
 23     584   97.5     108  9  AED00594                   Aed00594 Rhesus mo
 24   578.5   96.6     129  6  AAE36788                   Aae36788 Human Bv8
 25   578.5   96.6     129  7  ADJ71815                   Adj71815 Human pro
 26   578.5   96.6     129  8  ADN41864                   Adn41864 Amino aci
 27   578.5   96.6     129  8  ADS86984                   Ads86984 Human Zve
 28   578.5   96.6     129  8  ADS00458                   Ads00458 Human Bv8
 29   551.5   92.1     124  7  ADJ71808                   Adj71808 Human Bv8
 30   536.5   89.6     100  9  ADY86166                   Ady86166 Human Bv8
 31   531.5   88.7     107  5  ABG94401                   Abg94401 Rat GPCR
 32   531.5   88.7     107  5  ABB06962                   Abb06962 Rat G pro
 33   531.5   88.7     107  7  ADD69059                   Add69059 Rat Bv8-r
 34   531.5   88.7     107  8  ADS86500                   Ads86500 Rat BV8 p
 35     528   88.1     126  7  ADI60152                   Adi60152 Secreted
 36     528   88.1     126  7  ADJ71800                   Adj71800 Human pro
 37   527.5   88.1     107  5  ABG94408                   Abg94408 Mouse GPC
 38   527.5   88.1     107  6  AAE36790                   Aae36790 Mouse Bv8
 39   527.5   88.1     107  7  ADD69077                   Add69077 Murine Bv
 40   527.5   88.1     107  8  ADS00462                   Ads00462 Murine Bv
 41   527.5   88.1     107  8  ADS86502                   Ads86502 Murine BV
 42     507   84.6     128  7  ADJ71809                   Adj71809 Mouse Bv8
 43     461   77.0      81  5  ABG94398                   Abg94398 Human GPC
 44     461   77.0      81  5  AAO15530                   Aao15530 Human phy
 45     461   77.0      81  5  AAE24385                   Aae24385 Human pro
 46     461   77.0      81  7  ADD69041                   Add69041 Human Bv8
 47     461   77.0      81  7  ADO05356                   Ado05356 Human maj
 48     461   77.0      81  8  ADN43258                   Adn43258 Amino aci
 49     461   77.0      81  8  ADR24005                   Adr24005 Human ZAQ
 50     461   77.0      81  8  ADS86493                   Ads86493 Human BV8
 51     461   77.0      81  8  ADS75497                   Ads75497 Human pro
 52     461   77.0      81  9  ADW00755                   Adw00755 Amino aci
 53     461   77.0      81  9  ADZ88900                   Adz88900 Human pro
 54     461   77.0      81  9  ADZ58574                   Adz58574 Human ZAQ
 55     461   77.0      81  9  AEB45593                   Aeb45593 Human Zve
 56     461   77.0      81  9  AED00597                   Aed00597 Human pro
 57     456   76.1      80  5  ABG94400                   Abg94400 C-termina
 58     456   76.1      80  7  ADD69044                   Add69044 Human Bv8
 59     445   74.3      81  5  ABG94402                   Abg94402 Rat GPCR
 60     445   74.3      81  5  ABB06963                   Abb06963 Rat G pro


                                ALIGNMENTS
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OM protein - protein search, using sw model

Run on:         June 12, 2006, 20:16:57 ; Search time 51 Seconds
                                            (without alignments)
                                            185.359 Million cell updates/sec

Title:          US-10-680-800A-2
Perfect score:  599
Sequence:       1 MRSLCCAPLLLLLLLPPLLL..........LPGLACLRTSFNRFICLAQK 108

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:      650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :       Issued_Patents_AA:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                               SUMMARIES
                 %
Result          Query
  No.   Score   Match Length DB  ID                         Description
  ----------------------------------------------------------------------------
     1    599   100.0    108  2  US-09-712-529-2              Sequence 2, Appli
     2    599   100.0    108  2  US-10-212-201A-2             Sequence 2, Appli
     3    599   100.0    108  2  US-10-212-355-2              Sequence 2, Appli
     4    303    50.6    105  2  US-09-712-529-5              Sequence 5, Appli
     5    303    50.6    105  2  US-10-212-201A-5             Sequence 5, Appli
     6    303    50.6    105  2  US-10-212-355-5              Sequence 5, Appli
     7    303    50.6    105  2  US-09-991-181-371            Sequence 371, App
     8    303    50.6    105  2  US-09-990-444-371            Sequence 371, App
     9    303    50.6    105  2  US-09-997-333-371            Sequence 371, App
    10    303    50.6    105  2  US-09-992-598-371            Sequence 371, App
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 11     303    50.6     105  2  US-09-989-735-371          Sequence 371, App
 12     303    50.6     105  3  US-09-989-726-371          Sequence 371, App
 13     303    50.6     105  3  US-09-997-514-371          Sequence 371, App
 14     303    50.6     105  3  US-09-989-728-371          Sequence 371, App
 15     303    50.6     105  3  US-09-997-349-371          Sequence 371, App
 16     303    50.6     105  3  US-09-997-653-371          Sequence 371, App
 17     303    50.6     105  3  US-09-989-293A-371         Sequence 371, App
 18     296    49.4     105  2  US-09-621-976-5350         Sequence 5350, Ap
 19     268    44.7      80  2  US-09-513-999C-4698        Sequence 4698, Ap
 20   101.5    16.9     224  2  US-09-161-241-14           Sequence 14, Appl
 21     100    16.7     266  2  US-09-161-241-10           Sequence 10, Appl
 22     100    16.7     266  2  US-09-976-594-1086         Sequence 1086, Ap
 23     100    16.7     266  2  US-09-999-833A-456         Sequence 456, App
 24     100    16.7     266  2  US-10-020-445A-456         Sequence 456, App
 25     100    16.7     266  2  US-09-978-189-456          Sequence 456, App
 26     100    16.7     266  2  US-10-017-085A-456         Sequence 456, App
 27     100    16.7     266  3  US-10-145-129A-456         Sequence 456, App
 28     100    16.7     266  3  US-10-013-929A-456         Sequence 456, App
 29     100    16.7     266  3  US-10-013-917A-456         Sequence 456, App
 30      98    16.4     259  2  US-09-161-241-11           Sequence 11, Appl
 31      97    16.2     186  2  US-09-949-016-7146         Sequence 7146, Ap
 32      97    16.2     207  2  US-09-161-241-13           Sequence 13, Appl
 33      97    16.2     259  2  US-09-161-241-12           Sequence 12, Appl
 34      97    16.2     259  2  US-09-949-016-6872         Sequence 6872, Ap
 35      97    16.2     259  2  US-10-012-231A-70          Sequence 70, Appl
 36      97    16.2     259  2  US-10-015-389A-70          Sequence 70, Appl
 37      97    16.2     259  2  US-10-006-768A-70          Sequence 70, Appl
 38      97    16.2     259  2  US-10-015-671A-70          Sequence 70, Appl
 39      97    16.2     259  2  US-10-015-393A-70          Sequence 70, Appl
 40      97    16.2     259  2  US-10-011-833A-70          Sequence 70, Appl
 41      97    16.2     259  2  US-10-006-041A-70          Sequence 70, Appl
 42      97    16.2     259  2  US-10-012-064A-70          Sequence 70, Appl
 43      97    16.2     259  2  US-10-015-392A-70          Sequence 70, Appl
 44      97    16.2     259  3  US-10-011-795B-70          Sequence 70, Appl
 45      97    16.2     259  3  US-10-015-386A-70          Sequence 70, Appl
 46      97    16.2     259  3  US-10-012-121A-70          Sequence 70, Appl
 47      97    16.2     259  3  US-10-006-485A-70          Sequence 70, Appl
 48      97    16.2     259  3  US-10-006-746A-70          Sequence 70, Appl
 49      97    16.2     259  3  US-10-012-752A-70          Sequence 70, Appl
 50      97    16.2     259  3  US-10-017-253A-70          Sequence 70, Appl
 51      97    16.2     259  3  US-10-015-519A-70          Sequence 70, Appl
 52      97    16.2     259  3  US-10-015-715A-70          Sequence 70, Appl
 53      97    16.2     259  3  US-10-007-236A-70          Sequence 70, Appl
 54      95    15.9     350  2  US-09-161-241-9            Sequence 9, Appli
 55      95    15.9     350  2  US-09-907-794A-236         Sequence 236, App
 56      95    15.9     350  2  US-09-905-125A-236         Sequence 236, App
 57      95    15.9     350  2  US-09-902-775A-236         Sequence 236, App
 58      95    15.9     350  2  US-09-906-700-236          Sequence 236, App
 59      95    15.9     350  2  US-09-903-603A-236         Sequence 236, App
 60      95    15.9     350  2  US-09-904-920A-236         Sequence 236, App


                              ALIGNMENTS


RESULT 1
US-09-712-529-2
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OM protein - protein search, using sw model

Run on:         June 12, 2006, 20:12:02 ; Search time 39 Seconds
                                           (without alignments)
                                          266.446 Million cell updates/sec

Title:          US-10-680-800A-2
Perfect score:  599
Sequence:       1 MRSLCCAPLLLLLLLPPLLL..........LPGLACLRTSFNRFICLAQK 108

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :       PIR_80:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                   %
Result           Query
   No.   Score   Match Length DB  ID                        Description
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     1      95    15.9    350  2  JC7188                    REIC protein - hum
     2    76.5    12.8   1574  2  T13954                    MEGF6 protein - ra
     3      76    12.7   3712  2  S18253                    laminin alpha-1 ch
     4    75.5    12.6    264  2  T16271                    hypothetical prote
     5      75    12.5    257  2  I38025                    keratin-like prote
     6      75    12.5   1609  1  MMHUB2                    laminin gamma-1 ch
     7      74    12.4    593  1  GYHU                      granulin precursor
     8    73.5    12.3   2471  2  A49128                    cell-fate determin
     9      73    12.2    424  2  F95330                    hypothetical prote
    10      73    12.2   1522  2  H88380                    protein T22F7.3 [i
    11    72.5    12.1    212  2  S43601                    R07E5.4 protein (c
    12    72.5    12.1    214  2  A88427                    protein R07E5.4 [i
    13    71.5    11.9    112  1  XLHU                      colipase precursor
    14    71.5    11.9     565  2  T16408                          hypothetical prote
    15      71    11.9    1722  2  E89753                          protein F11C7.4 [i
    16      70    11.7     203  2  H75434                          hypothetical prote
    17      70    11.7     301  2  JC5846                          chitinase (EC 3.2.
    18      70    11.7     850  2  S56015                          gastric mucin MUC5
    19      70    11.7    1101  2  T16840                          hypothetical prote
    20    69.5    11.6      74  2  S25773                          testis-specific pr
    21    69.5    11.6     738  2  S40992                          hypothetical prote
    22    69.5    11.6     739  2  B88553                          protein K04H4.2b [
    23    69.5    11.6     802  2  T24293                          hypothetical prote
    24    69.5    11.6     949  2  T24294                          hypothetical prote
    25      69    11.5    1964  2  T09059                          notch4 - mouse
    26    68.5    11.4    1220  2  A56136                          jagged protein pre
    27      68    11.4     313  2  S08198                          cytochrome-c3 hydr
    28      68    11.4    1607  1  MMMSB2                          laminin gamma-1 ch
    29    67.5    11.3     314  1  HQDVSG                          cytochrome-c3 hydr
    30    67.5    11.3    1687  2  T30176                          EGF repeat transme
    31      67    11.2      82  2  S65779                          gamma-thionin prec
    32      67    11.2      83  2  T26545                          hypothetical prote
    33      67    11.2     155  2  A45293                          conopressin precur
    34    66.5    11.1     907  2  T27317                          hypothetical prote
    35    66.5    11.1    3075  2  S14458                          laminin alpha-1 ch
    36      66    11.0     112  2  I51909                          colipase precursor
    37      66    11.0     345  2  T25138                          hypothetical prote
    38      66    11.0     358  2  T25137                          hypothetical prote
    39      66    11.0    1955  1  AGCH                            agrin precursor -
    40    65.5    10.9     297  2  H69609                          hypothetical prote
    41    65.5    10.9     318  2  E87929                          protein T22H2.6 [i
    42    65.5    10.9     657  2  T49875                          probable amidase -
    43    65.5    10.9    1599  2  T16210                          hypothetical prote
    44    65.5    10.9    1620  2  T27283                          hypothetical prote
    45    65.5    10.9    2195  2  T34264                          hypothetical prote
    46      65    10.9     317  2  I46916                          insulin-like growt
    47      65    10.9     375  1  A60004                          matrix protein - m
    48      65    10.9     375  1  MFNZMS                          matrix protein - m
    49      65    10.9     589  2  C38128                          epithelin/granulin
    50      65    10.9     739  2  H85245                          VP1 like protein [
    51      65    10.9     739  2  T05163                          hypothetical prote
    52      65    10.9    4135  2  T42629                          tenascin-X - bovin
    53    64.5    10.8     250  1  A49053                          CD27 antigen precu
    54    64.5    10.8    2318  2  S45306                          notch 3 protein -
    55    64.5    10.8    3871  2  T22812                          hypothetical prote
    56      64    10.7     131  1  KRSHA3                          keratin high-sulfu
    57      64    10.7     602  2  S69198                          prostaglandin G/H
    58      64    10.7     922  2  T23573                          hypothetical prote
    59      64    10.7    1797  2  A55677                          laminin beta-2 cha
    60      64    10.7    4544  1  S02392                          alpha-2-macroglobu


                                   ALIGNMENTS


RESULT 1
JC7188
REIC protein - human
C;Species: Homo sapiens (man)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
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                        GenCore version 5.1.9
             Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:         June 12, 2006, 20:29:18 ; Search time 16 Seconds
                                           (without alignments)
                                          85.342 Million cell updates/sec

Title:          US-10-680-800A-2
Perfect score:  599
Sequence:       1 MRSLCCAPLLLLLLLPPLLL..........LPGLACLRTSFNRFICLAQK 108

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters:      64916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :       Published_Applications_AA_New:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
                %
Result          Query
   No.   Score  Match Length DB  ID                          Description
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     1     322   53.8     80  7  US-11-304-129-34             Sequence 34, Appl
     2     303   50.6    105  7  US-11-304-129-23             Sequence 23, Appl
     3     302   50.4    105  7  US-11-304-129-22             Sequence 22, Appl
     4     291   48.6     86  7  US-11-304-129-21             Sequence 21, Appl
     5     290   48.4     86  7  US-11-304-129-20             Sequence 20, Appl
     6     100   16.7    266  6  US-10-505-928-533            Sequence 533, App
     7      97   16.2    259  6  US-10-196-749-250            Sequence 250, App
     8      95   15.9    350  7  US-11-101-316-8              Sequence 8, Appli
     9    83.5   13.9     81  6  US-10-953-349-31814          Sequence 31814, A
 10       75   12.5     575  7  US-11-217-997-32              Sequence 32, Appl
 11       75   12.5    1418  7  US-11-217-997-38              Sequence 38, Appl
 12       75   12.5    1450  7  US-11-217-997-6               Sequence 6, Appli
 13       75   12.5    1547  7  US-11-217-997-22              Sequence 22, Appl
 14       75   12.5    1577  7  US-11-217-997-16              Sequence 16, Appl
 15       75   12.5    1577  7  US-11-217-997-20              Sequence 20, Appl
 16       75   12.5    1620  7  US-11-217-997-42              Sequence 42, Appl
 17       75   12.5    1653  7  US-11-217-997-40              Sequence 40, Appl
 18     71.5   11.9      69  6  US-10-953-349-31815           Sequence 31815, A
 19     71.5   11.9    1594  7  US-11-217-997-18              Sequence 18, Appl
 20     69.5   11.6    5738  6  US-10-505-928-150             Sequence 150, App
 21     66.5   11.1    1398  7  US-11-217-997-4               Sequence 4, Appli
 22     66.5   11.1    1403  7  US-11-217-997-12              Sequence 12, Appl
 23     66.5   11.1    1404  7  US-11-217-997-2               Sequence 2, Appli
 24       66   11.0     243  7  US-11-320-192-9               Sequence 9, Appli
 25       65   10.9     243  7  US-11-320-192-12              Sequence 12, Appl
 26     64.5   10.8     446  7  US-11-293-697-3580            Sequence 3580, Ap
 27     63.5   10.6     215  6  US-10-953-349-34480           Sequence 34480, A
 28     63.5   10.6     432  6  US-10-953-349-17477           Sequence 17477, A
 29       63   10.5    2026  6  US-10-505-928-831             Sequence 831, App
 30     62.5   10.4     342  7  US-11-038-753-1               Sequence 1, Appli
 31       62   10.4     491  7  US-11-217-997-30              Sequence 30, Appl
 32     61.5   10.3     236  6  US-10-953-349-33388           Sequence 33388, A
 33     61.5   10.3     261  6  US-10-953-349-33387           Sequence 33387, A
 34     61.5   10.3     333  6  US-10-953-349-33386           Sequence 33386, A
 35       61   10.2    3396  6  US-10-505-928-449             Sequence 449, App
 36     60.5   10.1     171  7  US-11-154-977-67              Sequence 67, Appl
 37     60.5   10.1     318  7  US-11-154-977-35              Sequence 35, Appl
 38     60.5   10.1    1300  6  US-10-196-749-269             Sequence 269, App
 39       60   10.0      82  6  US-10-953-349-36789           Sequence 36789, A
 40       60   10.0     152  6  US-10-953-349-16556           Sequence 16556, A
 41       60   10.0     359  7  US-11-336-497-11              Sequence 11, Appl
 42     59.5    9.9     228  6  US-10-953-349-38889           Sequence 38889, A
 43     59.5    9.9     256  6  US-10-953-349-15546           Sequence 15546, A
 44     59.5    9.9     318  6  US-10-953-349-30612           Sequence 30612, A
 45     59.5    9.9     366  6  US-10-953-349-30611           Sequence 30611, A
 46     59.5    9.9    1198  7  US-11-217-997-14              Sequence 14, Appl
 47       59    9.8      97  6  US-10-196-749-468             Sequence 468, App
 48       59    9.8     454  6  US-10-953-349-6483            Sequence 6483, Ap
 49       59    9.8     461  6  US-10-511-937-2945            Sequence 2945, Ap
 50       59    9.8     461  7  US-11-183-218-32              Sequence 32, Appl
 51       59    9.8     546  6  US-10-953-349-6482            Sequence 6482, Ap
 52       59    9.8     561  6  US-10-953-349-6481            Sequence 6481, Ap
 53       59    9.8    1674  6  US-10-511-937-2587            Sequence 2587, Ap
 54       59    9.8    4440  6  US-10-196-749-525             Sequence 525, App
 55     58.5    9.8     174  7  US-11-293-697-3348            Sequence 3348, Ap
 56     58.5    9.8     174  7  US-11-293-697-4753            Sequence 4753, Ap
 57     58.5    9.8     185  7  US-11-293-697-4579            Sequence 4579, Ap
 58     58.5    9.8     282  6  US-10-953-349-19704           Sequence 19704, A
 59     58.5    9.8     309  6  US-10-953-349-19703           Sequence 19703, A
 60     58.5    9.8     335  6  US-10-953-349-19702           Sequence 19702, A


                                  ALIGNMENTS


RESULT 1
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                         GenCore version 5.1.9
                Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:         June 12, 2006, 20:08:27 ; Search time 295 Seconds
                                           (without alignments)
                                           338.650 Million cell updates/sec

Title:          US-10-680-800A-2
Perfect score:  599
Sequence:       1 MRSLCCAPLLLLLLLPPLLL..........LPGLACLRTSFNRFICLAQK 108

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:      2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :       UniProt_7.2:*
                1:  uniprot_sprot:*
                2:  uniprot_trembl:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                      SUMMARIES
                  %
Result          Query
   No.   Score  Match Length DB  ID                          Description
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     1     599  100.0    108  2  Q6ISR0_HUMAN                Q6isr0 homo sapien
     2   578.5   96.6    129  1  PROK2_HUMAN                 Q9hc23 homo sapien
     3   578.5   96.6    129  2  Q53Z79_HUMAN                Q53z79 homo sapien
     4   531.5   88.7    107  1  PROK2_RAT                   Q8r413 rattus norv
     5     530   88.5    108  2  Q863H4_BOVIN                Q863h4 bos taurus
     6   522.5   87.2    107  2  Q50E38_9MURI                Q50e38 arvicanthis
     7   519.5   86.7    107  2  Q50E37_9MURI                Q50e37 arvicanthis
     8     511   85.3    128  2  Q6V8J7_RAT                  Q6v8j7 rattus norv
     9     510   85.1    128  2  Q863H5_BOVIN                Q863h5 bos taurus
    10     507   84.6    128  1  PROK2_MOUSE                 Q9qxu7 mus musculu
    11     502   83.8    128  2  Q50E34_9MURI                Q50e34 arvicanthis
    12     499   83.3    128  2  Q50E33_9MURI                Q50e33 arvicanthis
    13     386   64.4    104  2  Q2XXR8_VARVA                Q2xxr8 varanus var
    14     382   63.8    104  2  Q2XXR7_VARVA                Q2xxr7 varanus var
    15     353   58.9     82  2  Q2TBS7_BOVIN                Q2tbs7 bos taurus
    16   342.5    57.2      86  2  Q50E36_9MURI              Q50e36 arvicanthis
    17   339.5    56.7      86  2  Q50E35_9MURI              Q50e35 arvicanthis
    18   324.5    54.2     102  2  Q4SR12_TETNG              Q4sr12 tetraodon n
    19     322    53.8      81  1  VPRA_DENPO                P25687 dendroaspis
    20     303    50.6     105  1  PROK1_HUMAN               P58294 homo sapien
    21     303    50.6     105  2  Q5VWD4_HUMAN              Q5vwd4 homo sapien
    22     302    50.4     105  2  Q8TC69_HUMAN              Q8tc69 homo sapien
    23     299    49.9     105  1  PROK1_RAT                 Q8r414 rattus norv
    24     260    43.4      81  2  Q3ZFI2_BOVIN              Q3zfi2 bos taurus
    25   257.5    43.0      96  1  BV8_BOMVA                 Q9pw66 bombina var
    26   257.5    43.0      96  2  Q8JFQ0_BOMMX              Q8jfq0 bombina max
    27     257    42.9      81  2  Q8K457_MOUSE              Q8k457 mus musculu
    28   253.5    42.3      96  2  Q5W280_BOMOR              Q5w280 bombina ori
    29   242.5    40.5      96  2  Q8JFE6_BOMMX              Q8jfe6 bombina max
    30   241.5    40.3      96  2  Q8JFX9_BOMMX              Q8jfx9 bombina max
    31   241.5    40.3      96  2  Q8JFY1_BOMMX              Q8jfy1 bombina max
    32     239    39.9      96  2  Q8JFY0_BOMMX              Q8jfy0 bombina max
    33   234.5    39.1      96  2  Q8JFX8_BOMMX              Q8jfx8 bombina max
    34     229    38.2     106  2  Q4RVU3_TETNG              Q4rvu3 tetraodon n
    35   227.5    38.0      96  2  Q8JFY2_BOMMX              Q8jfy2 bombina max
    36   126.5    21.1     124  2  Q56R10_PENMO              Q56r10 penaeus mon
    37   112.5    18.8     221  1  DKK4_MOUSE                Q8vej3 mus musculu
    38   110.5    18.4     104  2  Q56R11_PACLE              Q56r11 pacifastacu
    39     110    18.4      96  2  Q8UUX3_CHICK              Q8uux3 gallus gall
    40   108.5    18.1     256  2  Q5EHU6_GECJA              Q5ehu6 gecko japon
    41     103    17.2     180  2  Q4RJF1_TETNG              Q4rjf1 tetraodon n
    42     103    17.2     272  1  DKK1_MOUSE                O54908 mus musculu
    43     103    17.2     272  2  Q80UL5_MOUSE              Q80ul5 m dickkopf
    44   101.5    16.9     224  1  DKK4_HUMAN                Q9ubt3 homo sapien
    45   101.5    16.9     224  2  Q3KNX0_HUMAN              Q3knx0 homo sapien
    46     101    16.9      39  2  Q50E61_9MURI              Q50e61 arvicanthis
    47   100.5    16.8      31  2  Q50E40_9MURI              Q50e40 arvicanthis
    48     100    16.7     240  2  Q9PWH3_BRARE              Q9pwh3 brachydanio
    49     100    16.7     266  1  DKK1_HUMAN                O94907 homo sapien
    50      99    16.5     110  2  Q4PML0_IXOSC              Q4pml0 ixodes scap
    51      99    16.5     255  2  Q9DDA4_XENLA              Q9dda4 xenopus lae
    52      98    16.4     259  1  DKK2_MOUSE                Q9qyz8 mus musculu
    53      98    16.4     259  2  Q8BFW0_MOUSE              Q8bfw0 m 10, 11 da
    54      98    16.4     268  2  Q6PVU5_RABIT              Q6pvu5 oryctolagus
    55    97.5    16.3      31  2  Q50E39_9MURI              Q50e39 arvicanthis
    56      97    16.2     259  1  DKK2_HUMAN                Q9ubu2 homo sapien
    57      95    15.9     171  2  O43532_HUMAN              O43532 homo sapien
    58      95    15.9     341  2  Q5R8T0_PONPY              Q5r8t0 pongo pygma
    59      95    15.9     350  1  DKK3_HUMAN                Q9ubp4 homo sapien
    60      95    15.9     350  2  Q4R4I7_MACFA              Q4r4i7 macaca fasc


                                  ALIGNMENTS


RESULT 1
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AC   Q6ISR0;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   21-FEB-2006, entry version 6.
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